Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1 – 75. (canceled)

76. (currently amended) ~~A method of claim 69,~~ A method for developing nucleotide probes for myctophid fishes, said method comprising the steps of:

(i) extracting DNA from the muscle tissue of a myctophid fish,

(ii) selecting a gene region in the extracted DNA as a DNA template and amplifying the selected gene region with the a pair of forward and backward selected primers using polymerase chain reaction (PCR),

(iii) eluting the amplified DNA containing the selected gene region,

(iv) re-amplifying and re-eluting the amplified DNA in step (iii),

(v) cycle sequencing the of eluted DNA containing the selected gene region using a single primer to produce an extension product,

(vi) purifying the extension product containing the selected gene region,

(vii) sequencing the nucleotides of the extension product of step (vi) on an acrylamide gel,

(viii) confirming the nucleotide sequence of the selected gene region by Blast-Email,

(ix) ligating the extension product containing the selected gene region as a DNA insert into a cloning vector,

(x) preparing host cells for electro-transformation,

(xi) electro-transforming the host cells with the vector-containing DNA insert,

(xii) growing and harvesting of transformed host cells ,

(xiii) re-inoculating and growing transformed host cells that appear as white colonies and that express the DNA insert containing the selected gene region;

(xiv) confirming the presence of the DNA insert containing the selected gene region by polymerase chain reaction,

(xv) purifying the cloned DNA insert containing the selected gene region from the transformed host cells to produce a DNA probe,

(xvi) checking the purity and specificity of the DNA probe by cutting with a restriction enzyme,

(xvii) confirming the molecular size of the DNA probe,

(xviii) amplifying the DNA probe using the selected set of forward and backward primers of step (ii),

(xix) eluting the amplified DNA probe containing the selected gene region,

(xx) cycle sequencing the eluted DNA probe in step (xix) using a single set of primer,

(xxi) sequencing the eluted DNA probe in step (xix) on an acrylamide gel,

(xxii) comparing the nucleotide sequence of the DNA probe using "BLAST program" against the known sequences of similar genes in the genome data bases,

(xxiii) confirming the sequence of the DNA probe by aligning with sequence obtained in step (vii), and

(xxiv) designing species specific primers based on the sequence of the DNA probe, wherein the DNA probe for the D-Loop gene is PSL PROL, wherein the nucleotide base sequence of PSL PROL comprises: (750 BP) (SEQ ID NO:44)

5' CCTTTTCGGN ATAGGCCCAN CTCAAATGAA TTCCTTCTCT CCTGGTCCAA
GCCCAAACTG TGGACGGCAG GTTGACAATG GTTACAAATC GTGACAAATC
GGCTACATAA TTGCCGATAG CGATGTCGTC AAACCAAGTC AAACAATGGC
CGATGTATAT CGGCCAAACC CATATATGGG TCTGGCTGTA GTTTGTGTTG
AGCAACGTCA CACCAGTGTC TGGTCAGCAT ATAAGATGTT GACATCTTGC
AACATCTTAC CCACAGACAG ACAGTTACGG CTGCTTACGA ANGGCGCTAG
TGTTGTGGTG AGAAACGAAG ATACATACGT CAAACAGACG CCGGTGCACT
TGAAGACACT GTTTGAAGGT GCCGCACTAC TTGACAGACA GCCCATGATG
CGCTGGACAG TGACCAAAGC TACNGGAGGA CCANATGGAA ATCCTGTTGG
CGTTGCCGTG GGACTCAAGT TGTACACTTT TGGATGGTTG ATCACTANAN
CCGCTGCCGG GAGAAGCACT CGCTCCTGGT TCACTAATCA GATTGAGGTT
AACCANATTG ANGTAAACAT CTTCAACACA GTGTCTTTAT GCTGGATGAA
ATTNAGCCCA CNGGACACCA NAAAAGAATT NCCNCTGGTT CTNNCGGGGG
NCCCCNNNAA CGNNTNTTCC CCTTNTCTCN NNNGCGGNGA AGTTNCCCCC
CCCCACTNAN NTCTTCCTTC AANANNTTTC CNCCNNNAGA GGTTTTCCCN 3'.

77 - 107. (canceled)

108. (new) A polynulcleotide sequence comprising SEQ ID NO: 44.